

IN THE SPECIFICATION:

The following amendments are made pursuant to "Amendments In A Revised Format Now Permitted", 1267 Off. Gaz. Pat. Office 106 (February 25, 2003).

Please replace the title, beginning at page 1, line 1 of the specification, with the following rewritten title:

~~-- HUMAN GENOME DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GENE EXPRESSION ANALYSIS METHODS FOR MANUFACTURING CUSTOMER-DESIGNED SINGLE EXON MICROARRAYS --~~

Please replace the paragraph beginning at page 1, line 7, with the following rewritten paragraph:

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-- This application is a continuation-in-part of International Application No. PCT/US01/00666, filed January 30, 2001; is a continuation-in-part of International Application No. PCT/US01/00667, filed January 30, 2001; is a continuation-in-part of International Application No. PCT/US01/00664, filed January 30, 2001; is a continuation-in-part of International Application No. PCT/US01/00669, filed January 30, 2001; is a continuation-in-part of International Application No. PCT/US01/00665, filed January 30, 2001; is a continuation-in-part of International Application No. PCT/US01/00668, filed January 30, 2001; is a continuation-in-part of International Application No. PCT/US01/00663, filed January 30, 2001; is a continuation-in-part of International Application No. PCT/US01/00662, filed January 30, 2001; is a continuation-in-part of International Application No. PCT/US01/00661, filed

January 30, 2001; is a continuation-in-part of International Application No. PCT/US01/00670, filed January 30, 2001; ~~claims priority under 35 U.S.C. § 365(c) to international patent application nos. PCT/US01/00666, PCT/US01/00667, PCT/US01/00664, PCT/US01/00669, PCT/US01/00665, PCT/US01/00668, PCT/US01/00663, PCT/US01/00662, PCT/US01/00661, PCT/US01/00670, all filed January 30, 2001; claims the benefit of priority under 35 U.S.C. § 119(c) to provisional applications for United States Patent serial nos. 60/180,312, filed February 4, 2000, U.S. Provisional Application No. 60/207,456, filed May 26, 2000, U.S. Provisional Application No. 60/234,687, filed September 21, 2000, and U.S. Provisional Application No. 60/236,359, filed September 27, 2000; claims priority under 35 U.S.C. § 119(a) to GB 24263.6, filed October 4, 2000; is a continuation-in-part of U.S. Application No. 09/608,408, filed June 30, 2000; is a continuation-in-part of U.S. Application No. 09/632,366, filed August 3, 2000, which claims the benefit of U.S. Provisional Application No. 60/180,312, filed February 4, 2000, and U.S. Provisional Application No. 60/207,456, filed May 26, 2000; and is a continuation-in-part of U.S. Application No. 09/774,203, filed January 29, 2001, which is a continuation-in-part of U.S. Application No. 09/608,408, filed June 30, 2000, is a continuation-in-part of U.S. Application No. 09/632,366, filed August 3, 2000, claims the benefit of U.S. Provisional Application No. 60/180,312, filed February 4, 2000, U.S. Provisional Application No. 60/207,456, filed May 26, 2000, U.S. Provisional Application No. 60/234,687, filed September 21, 2000, and U.S. Provisional Application No. 60/236,359, filed September 27, 2000, and claims priority under~~

35 U.S.C. § 119(a) to GB 24263.6, filed October 4, 2000, ~~and is a continuation in part of United States patent application serial nos. 09/608,408, filed June 30, 2000, 09/632,366, filed August 3, 2000, and 09/774,203, filed January 29, 2001, the disclosures of which are incorporated herein by reference in their entireties.~~

Please replace the paragraph beginning at page 91, line 32, with the following rewritten paragraph:

--Identification can be effected by comparing the genomic sequence returned by query 20 with public or private databases containing known repetitive sequence, vector sequence, artificial sequence, and other artifactual sequence. Such comparison can readily be done using programs well known in the art, such as CROSS_MATCH or REPEATMASKER, the latter available on-line at the University of Washington Genome Center web site ~~<http://ftp.genome.washington.edu/RM/RepeatMasker.html>~~, or by proprietary sequence comparison programs the engineering of which is well within the skill in the art.--

Please replace the paragraph beginning at page 159, line 11, with the following rewritten paragraph:

--For purposes herein, percent identity of two nucleic acid sequences is determined using the procedure of Tatiana et al., "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", *FEMS Microbiol Lett.* 174:247-250 (1999), which procedure is effectuated by the

computer program BLAST 2 SEQUENCES, available online at the
National Center for Biotechnology Information (NCBI) website.

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~~<http://www.ncbi.nlm.nih.gov/blast/bl2seq/bl2.html>~~ --